



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of
Mature Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 Cambridge Park Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: United States of America
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 07/621092
(B) FILING DATE: 26-NOV-1990
(C) CLASSIFICATION: 424

(vii) PRIOR APPLICATION DATA: not applicable

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Ellen J. Kapinos, Esquire
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI 5181

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 876-1170
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(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) Topology: unknown

(ii) MOLECULE TYPE: partial human genomic DNA

- (A) DESCRIPTION: sequence encoding furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouwe land et al, Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATG GAG CTC AGG CCC TGG TTC	21
Met Glu Leu Arg Pro Trp Leu	
1 5	

CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA	60
Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu	
10 15 20	

GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG	99
Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr	
25 30	

TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC	138
Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn	
35 40 45	

AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG	177
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln	
50 55	

ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG	216
Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val	
60 65 70	

ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC	255
Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser	
75 80 85	
CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG	294
Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln	
90 95	
CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG	333
Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln	
100 105 110	
GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG	372
Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu	
115 120	
TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC	411
Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala	
125 130 135	
TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC	450
Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser	
140 145 150	
ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG	489
Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu	
155 160	
GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT	528
Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn	
165 170 175	
GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG	567
Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met	
180 185	
AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG	606
Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val	
190 195 200	
GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG	645
Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val	
205 210 215	
GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT	684
Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp	
220 225	
GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC	723
Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly	
230 235 240	
CTG AAC CCC AAC CAC ATC CAC ATC TAC AGT GCC AGC TGG	762

Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp		
				245				250						
GGC	CCC	GAG	GAT	GAC	GGC	AAG	ACA	GTG	GAT	GGG	CCA	GCC	801	
Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala		
255					260				265					
CGG	CTC	GCC	GAG	GAG	GCC	TTC	TTC	CGT	GGG	CTT	AGC	CAG	840	
Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln		
	270					275				280				
GGC	CGA	GGG	GGG	CTG	GGC	TCC	ATC	TTT	GTC	TGG	GCC	TCG	879	
Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser		
				285				290						
GGG	AAC	GGG	GGG	CGG	GAA	CAT	GAC	AGC	TGC	AAC	TGC	GAC	918	
Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp		
	295					300			305					
GGC	TAC	ACC	AAC	AGT	ATC	TAC	ACG	CTG	TCC	ATC	AGC	AGC	957	
Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser		
	310					315								
GCC	ACG	CAG	TTT	GGC	AAC	GTG	CCG	TGG	TAC	AGC	GAG	GCC	996	
Ala	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala		
	320				325				330					
TGC	TCG	TCC	ACA	CTG	GCC	ACG	ACC	TAC	AGC	AGT	GGC	AAC	1035	
Cys	Ser	Ser	Thr	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn		
	335					340				345				
CAG	AAT	GAG	AAG	CAG	ATC	GTG	ACG	ACT	GAC	TTG	CGG	CAG	1074	
Gln	Asn	Glu	Lys	Gln	Ile	Val	Thr	Thr	Asp	Leu	Arg	Gln		
				350				355						
AAG	TGC	ACG	GAG	TCT	CAC	ACG	GGC	ACC	TCA	GCC	TCT	GCC	1113	
Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala		
	360					365				370				
CCC	TTA	GCA	GCC	GGC	ATC	ATT	GCT	CTC	ACC	CTG	GAG	GCC	1152	
Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala		
				375				380						
AAT	AAG	AAC	CTC	ACA	TGG	CGG	GAC	ATG	CAA	CAC	CTG	GTG	1191	
Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val		
	385				390				395					
GTA	CAG	ACC	TCG	AAG	CCA	GCC	CAC	CTC	AAT	GCC	AAC	GAC	1230	
Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp		
				400			405			410				
TGG	GCC	ACC	AAT	GGT	GTG	GGG	CGG	AAA	GTG	AGC	CAC	TCA	1269	
Trp	Ala	Thr	Asn	Gly	Val	Gly	Arg	Lys	Val	Ser	His	Ser		
				415				420						

TAT	GGC	TAC	GGG	CTT	TTC	GAC	GCA	GGC	GCC	ATG	GTG	GCC	1308	
Tyr	Gly	Tyr	Gly	Leu	Leu	Asp	Ala	Gly	Ala	Met	Val	Ala		
425						430					435			
CTG	GCC	CAG	AAT	TGG	ACC	ACA	GTC	GCC	CCC	CAG	CGG	AAG	1347	
Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	Lys		
					440				445					
TGC	ATC	ATC	GAC	ATC	CTC	ACC	GAG	CCC	AAA	GAC	ATC	GGG	1386	
Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly		
450					455				460					
AAA	CGG	CTC	GAC	CTC	CGG	AAC	ACC	GTG	ACC	GCG	TCC	CTG	1425	
Lys	Arg	Leu	Glu	Val	Arg	Lys	Thr	Val	Thr	Ala	Cys	Leu		
					465			470		475				
GGC	GAG	CCC	AAC	CAC	ATC	ACT	CGG	CTG	GAG	CAC	GCT	CAG	1464	
Gly	Glu	Glu	Pro	Asn	His	Ile	Thr	Arg	Leu	Glu	His	Ala	Gln	
					480				485					
GCG	CGG	CTC	ACC	CTG	TCC	TAT	AAT	CGC	CGT	GGC	GAC	CTG	1503	
Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	Arg	Arg	Gly	Asp	Leu		
					490		495			500				
GCC	ATC	CAC	CTG	GTC	AGC	CCC	ATG	GGC	ACC	CGC	TCC	ACC	1542	
Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	Ser	Thr		
					505			510						
CTG	CTG	GCA	GCC	AGG	CCA	CAT	GAC	TAC	TCC	GCA	GAT	GGG	1581	
Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly		
					515		520			525				
TTT	AAT	GAC	TGG	GCC	TTC	ATG	ACA	ACT	CAT	TCC	TGG	GAT	1620	
Phe	Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp		
					530		535			540				
GAC	GAT	CCC	TCT	GGG	GAG	TGG	GTC	CTA	GAG	ATT	GAA	AAC	1659	
Glu	Asp	Pro	Ser	Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn		
					545				550					
ACC	AGC	GAA	GCC	AAC	AAC	TAT	GGG	ACG	CTG	ACC	AAC	TCC	1698	
Thr	Ser	Glu	Ala	Asn	Asn	Tyr	Gly	Thr	Leu	Thr	Lys	Phe		
					555		560			565				
ACC	CTC	GTA	CTC	TAT	GGC	ACC	GCC	CCT	GAC	GGG	CTC	CCC	1737	
Thr	Leu	Val	Leu	Tyr	Gly	Thr	Ala	Pro	Glu	Gly	Leu	Pro		
					570			575						
GTA	CCT	CCA	GAA	AGC	AGT	GGC	TGC	AAG	ACC	CTC	ACG	TCC	1776	
Val	Pro	Pro	Glu	Ser	Ser	Gly	Cys	Lys	Thr	Leu	Thr	Ser		
					580		585			590				
AGT	CAG	GCC	TGT	GTG	GTG	TGC	GAG	GAA	GGC	TTC	TCC	CTC	1815	
Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu		

595

600

605

CAC	CAG	AAG	AGC	TGT	GTC	CAG	CAC	TGC	CCT	CCA	GGC	TTC	1854
His	Gln	Lys	Ser	Cys	Val	Gln	Asn	Cys	Pro	Pro	Gly	Phe	
				610				615					
GCC	CCC	CAA	GTC	CTC	GAT	ACG	CAC	TAT	AGC	ACC	GAG	AAT	1893
Ala	Pro	Gln	Val	Leu	Asp	Thr	Asn	Tyr	Ser	Thr	Glu	Asn	
				620		625		630					
GAC	GTG	GAG	ACC	ATC	CGG	GCC	AGC	GTC	TGC	GCC	CCC	TGC	1932
Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val	Cys	Ala	Pro	Cys	
				635		640							
CAC	GCC	TCA	TGT	GCC	ACA	TGC	CAG	GGG	CCG	GCC	CTG	ACA	1971
His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu	Thr	
				645		650		655					
GAC	TGC	CTC	AGC	TGC	CCC	AGC	CAC	GCC	TCC	TTG	GAC	CCT	2010
Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro	
				660		665		670					
GTG	GAG	CAG	ACT	TGC	TCC	CGG	CAA	AGC	CAG	AGC	AGC	CGA	2049
Val	Glu	Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg	
				675		680							
GAG	TCC	CCG	CCA	CAG	CAG	CAG	CCA	CCT	CGG	CTG	CCC	CCG	2088
Glu	Ser	Pro	Pro	Gln	Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro	
				685		690		695					
GAG	GTG	GAG	GCG	GGG	CAA	CGG	CTG	CGG	GCA	GGG	CTG	CTG	2127
Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu	Arg	Ala	Gly	Leu	Leu	
				700		705							
CCC	TCA	CAC	CTG	CCT	GAG	GTG	GTG	GCC	GGC	CTC	AGC	TGC	2166
Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu	Ser	Cys	
				710		715		720					
GCC	TTC	ATC	GTG	CTG	GTC	TTC	GTC	ACT	GTC	TTC	CTG	CTC	2205
Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Val	
				725		730		735					
CTG	CAG	CTG	CGC	TCT	GGC	TTT	AGT	TTT	CGG	GGG	GTG	AAG	2244
Leu	Gln	Leu	Arg	Ser	Gly	Phe	Ser	Phe	Arg	Gly	Val	Lys	
				740		745							
GTG	TAC	ACC	ATG	GAC	CGT	GGC	CTC	ATC	TCC	TAC	AAG	GGG	2283
Val	Tyr	Thr	Met	Asp	Arg	Gly	Leu	Ile	Ser	Tyr	Lys	Gly	
				750		755		760					
CTG	CCC	CCT	GAA	GCC	TGG	CAG	GAG	GAG	TGC	CCG	TCT	GAC	2322
Leu	Pro	Pro	Glu	Ala	Trp	Gln	Glu	Glu	Cys	Pro	Ser	Asp	
				765		770							

TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT 2361
Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
775 780 785

ATC AAA GAC CAG AGC GCC CTC TGA 2385
Ile Lys Asp Gln Ser Ala Leu End
790

(3) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) Topology: unknown

(ii) MOLECULE TYPE: furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouwehand et al,
Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Met Glu Leu Arg Pro Trp Leu
1 5

Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
10 15 20

Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
25 30

Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
35 40 45

Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
50 55

Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val
60 65 70

Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
75 80 85

Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln
90 95

Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln
100 105 110

Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu
115 120

Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala
125 130 135

Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser
140 145 150

Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu
155 160

Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
165 170 175

Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met
180 185

Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val
190 195 200

Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val
205 210 215

Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp
220 225

Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly
230 235 240

Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp
245 250

Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala
255 260 265

Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln
270 275 280

Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
285 290

Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
295 300 305

Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
310 315

Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
320 325 330

Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
335 340 345

Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
350 355

Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
360 365 370

Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
375 380

Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
385 390 395

Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
400 405 410

Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
415 420

Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
425 430 435

Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
440 445

Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
450 455 460

Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
465 470 475

Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
480 485

Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
490 495 500

Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
505 510

Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
515 520 525

Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
530 535 540

Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
545 550

Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
555 560 565

Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
570 575

Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
580 585 590

Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
595 600 605

His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
610 615

Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
620 625 630

Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
635 640

His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
645 650 655

Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
660 665 670

Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
675 680

Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
685 690 695

Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
700 705

Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
710 715 720

Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
725 730 735

Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
740 745

Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
750 755 760

Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
765 770

Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
775 780 785

Ile Lys Asp Gln Ser Ala Leu
790